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## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/521,384  
Source: PCT  
Date Processed by STIC: 10/25/2005

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PCT

## RAW SEQUENCE LISTING

DATE: 10/25/2005

PATENT APPLICATION: US/10/521,584

TIME: 13:39:55

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Output Set: N:\CRF4\10252005\J521584.raw

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4 <110> APPLICANT: REINDL, ANDREAS
6 <120> TITLE OF INVENTION: NADH-DEPEDENT CYTOCHROME b5 REDUCTASE AS TARGET FOR
HERBICIDES
8 <130> FILE REFERENCE: BASF.10029
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,584
C--> 11 <141> CURRENT FILING DATE: 2005-01-18
13 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07590
14 <151> PRIOR FILING DATE: 2003-07-14
16 <150> PRIOR APPLICATION NUMBER: DE 102 32 778
17 <151> PRIOR FILING DATE: 2002-07-18
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn version 3.1
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26 <213> ORGANISM: Arabidopsis thaliana
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37 gtc ttc gtt gct ttc gtc gcc gtt ggt gct ggt gct gct tat ttt ctt      96
38 Val Phe Val Ala Phe Val Ala Val Gly Ala Gly Ala Ala Tyr Phe Leu
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41 aca tcc tcc aag aaa cgc aga gtg tgt ttg gat cca gag aat ttc aag      144
42 Thr Ser Ser Lys Lys Arg Arg Val Cys Leu Asp Pro Glu Asn Phe Lys
43          35          40          45
45 gag ttc aag ctt gtt aag aga cat cag ctt agt cac aat gtg gcc aag      192
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47          50          55          60
49 ttc gtt ttt gaa ctc cca act tct act tct gtg ttg ggt ctt ccc att      240
50 Phe Val Phe Glu Leu Pro Thr Ser Thr Ser Val Leu Gly Leu Pro Ile
51 65          70          75          80
53 gga caa cac atc agt tgc agg gga aag gat ggt caa gga gag gat gtt      288
54 Gly Gln His Ile Ser Cys Arg Gly Lys Asp Gly Gln Gly Glu Asp Val
55          85          90          95
57 att aag cca tac acc ccg act acg tta gac tct gac gtt gga cgt ttc      336
58 Ile Lys Pro Tyr Thr Pro Thr Thr Leu Asp Ser Asp Val Gly Arg Phe
59          100          105          110
61 gaa ctt gtc att aag atg tat ccg caa gga cgg atg tct cat cat ttc      384
62 Glu Leu Val Ile Lys Met Tyr Pro Gln Gly Arg Met Ser His His Phe
63          115          120          125

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66 Arg Glu Met Arg Val Gly Asp His Leu Ala Val Lys Gly Pro Lys Gly
67      130                      135                      140
69 agg ttc aag tat caa cca ggt cag ttt agg gca ttt gga atg ctt gct      480
70 Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala
71 145                      150                      155                      160
73 gga ggt tca ggc atc act ccc atg ttc caa gtg gcc aga gca att cta      528
74 Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu
75                      165                      170                      175
77 gaa aac cca aca gac aag aca aag gtg cat ctc att tac gcc aac gtc      576
78 Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val
79                      180                      185                      190
81 aca tac gac gac att ctc ttg aag gaa gaa ttg gag ggt ctt act acc      624
82 Thr Tyr Asp Asp Ile Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr
83                      195                      200                      205
85 aat tac cct gaa caa ttt aaa atc ttc tat gtt ttg aac cag cct ccg      672
86 Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro
87      210                      215                      220
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90 Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln
91 225                      230                      235                      240
93 act cat tgc cct gca cct gca tct gat att cag atc cta aga tgc gga      768
94 Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly
95                      245                      250                      255
97 cca ccg cca atg aac aag gcc atg gct gca aac ctt gaa gct ctg gga      816
98 Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly
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116      20                      25                      30
118 Thr Ser Ser Lys Lys Arg Arg Val Cys Leu Asp Pro Glu Asn Phe Lys
119      35                      40                      45
121 Glu Phe Lys Leu Val Lys Arg His Gln Leu Ser His Asn Val Ala Lys
122      50                      55                      60
124 Phe Val Phe Glu Leu Pro Thr Ser Thr Ser Val Leu Gly Leu Pro Ile
125 65                      70                      75                      80
127 Gly Gln His Ile Ser Cys Arg Gly Lys Asp Gly Gln Gly Glu Asp Val
128      85                      90                      95
130 Ile Lys Pro Tyr Thr Pro Thr Thr Leu Asp Ser Asp Val Gly Arg Phe
131      100                      105                      110

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139 Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala
140 145      150      155      160
142 Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu
143      165      170      175
145 Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val
146      180      185      190
148 Thr Tyr Asp Asp Ile Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr
149      195      200      205
151 Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro
152      210      215      220
154 Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln
155 225      230      235      240
157 Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly
158      245      250      255
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179 1      5      10      15
181 aca caa ata agc cac aat gtt gca aag ttc aga ttt gaa ctc ccc aca      96
182 Thr Gln Ile Ser His Asn Val Ala Lys Phe Arg Phe Glu Leu Pro Thr
183      20      25      30
185 cct act tct gta ttg ggc cta ccc att gga caa cat att agt tgc agg      144
186 Pro Thr Ser Val Leu Gly Leu Pro Ile Gly Gln His Ile Ser Cys Arg
187      35      40      45
189 ggc aag gat agt caa ggt gaa gag gtt gtt aaa ccg tac aca cca act      192
190 Gly Lys Asp Ser Gln Gly Glu Glu Val Val Lys Pro Tyr Thr Pro Thr
191      50      55      60
193 act ttg gat tca gat gtt gga tat ttt gaa cta gtt att aag atg tat      240
194 Thr Leu Asp Ser Asp Val Gly Tyr Phe Glu Leu Val Ile Lys Met Tyr
195 65      70      75      80
197 cct caa gga agg atg tct cat cat ttc cga gaa atg cgt gag ggt gat      288
198 Pro Gln Gly Arg Met Ser His His Phe Arg Glu Met Arg Glu Gly Asp
199      85      90      95
201 tat ttg gct gtg aag gga cct aag ggc cgc ttt aag tac cag cct ggc      336

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202 Tyr Leu Ala Val Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln Pro Gly
203          100          105          110
205 caa gtg aga gca ttt gga atg ctt gct gga ggc tct ggc att acc cca      384
206 Gln Val Arg Ala Phe Gly Met Leu Ala Gly Gly Ser Gly Ile Thr Pro
207          115          120          125
209 atg ttt cag gtt gct aga gct att ctc gaa aat cca aat gac aag aca      432
210 Met Phe Gln Val Ala Arg Ala Ile Leu Glu Asn Pro Asn Asp Lys Thr
211          130          135          140
213 aag gtg cac ttg ata tat gct aat gtt acc tat gaa gac ata ctt tta      480
214 Lys Val His Leu Ile Tyr Ala Asn Val Thr Tyr Glu Asp Ile Leu Leu
215 145          150          155          160
217 aag gaa cag ttg gat ggc ctt gct gct aac tat cct gac cgt ttc aaa      528
218 Lys Glu Gln Leu Asp Gly Leu Ala Ala Asn Tyr Pro Asp Arg Phe Lys
219          165          170          175
221 att tat tac gta ctg aat cag cct cct gaa gta tgg agc ggt ggt gtt      576
222 Ile Tyr Tyr Val Leu Asn Gln Pro Pro Glu Val Trp Ser Gly Gly Val
223          180          185          190
225 gga ttt gtg tcc aag gaa atg att cag act cat tgt cct gcc ccg gca      624
226 Gly Phe Val Ser Lys Glu Met Ile Gln Thr His Cys Pro Ala Pro Ala
227          195          200          205
229 tct gac att cag ata ctg agg tgt ggt cca cct cca atg aac aag gct      672
230 Ser Asp Ile Gln Ile Leu Arg Cys Gly Pro Pro Pro Met Asn Lys Ala
231          210          215          220
233 atg gct gct cat ctt gaa gcc ctt gga tac acc cca gag atg caa ttc      720
234 Met Ala Ala His Leu Glu Ala Leu Gly Tyr Thr Pro Glu Met Gln Phe
235 225          230          235          240
237 cag ttt taa      729
238 Gln Phe
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252          20          25          30
254 Pro Thr Ser Val Leu Gly Leu Pro Ile Gly Gln His Ile Ser Cys Arg
255          35          40          45
257 Gly Lys Asp Ser Gln Gly Glu Glu Val Val Lys Pro Tyr Thr Pro Thr
258          50          55          60
260 Thr Leu Asp Ser Asp Val Gly Tyr Phe Glu Leu Val Ile Lys Met Tyr
261 65          70          75          80
263 Pro Gln Gly Arg Met Ser His His Phe Arg Glu Met Arg Glu Gly Asp
264          85          90          95
266 Tyr Leu Ala Val Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln Pro Gly
267          100          105          110
269 Gln Val Arg Ala Phe Gly Met Leu Ala Gly Gly Ser Gly Ile Thr Pro
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272 Met Phe Gln Val Ala Arg Ala Ile Leu Glu Asn Pro Asn Asp Lys Thr
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275 Lys Val His Leu Ile Tyr Ala Asn Val Thr Tyr Glu Asp Ile Leu Leu
276 145                      150                      155                      160
278 Lys Glu Gln Leu Asp Gly Leu Ala Ala Asn Tyr Pro Asp Arg Phe Lys
279                      165                      170                      175
281 Ile Tyr Tyr Val Leu Asn Gln Pro Pro Glu Val Trp Ser Gly Gly Val
282                      180                      185                      190
284 Gly Phe Val Ser Lys Glu Met Ile Gln Thr His Cys Pro Ala Pro Ala
285                      195                      200                      205
287 Ser Asp Ile Gln Ile Leu Arg Cys Gly Pro Pro Pro Met Asn Lys Ala
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315 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Primer
317 <400> SEQUENCE: 6
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323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
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**VERIFICATION SUMMARY**

DATE: 10/25/2005

PATENT APPLICATION: US/10/521,584

TIME: 13:39:56

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date